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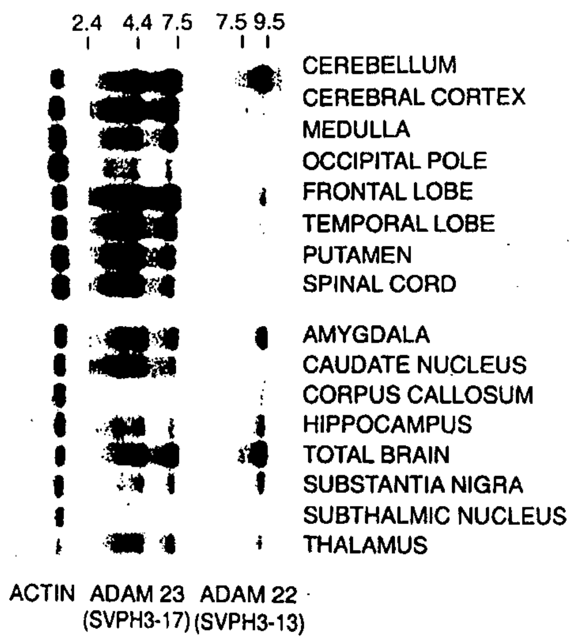
Without international search report and to be republished upon receipt of that report.

(54) Title: METALLOPROTEASE-DISINTEGRINS SVPH3-13 AND SVPH3-17 DNA AND POLYPEPTIDES

(57) Abstract

The invention is directed to purified and isolated novel SVPH3-13 or SVPH3-17 polypeptides, the nucleic acids encoding such polypeptides, processes for production of recombinant forms of such polypeptides, antibodies generated against these polypeptides, fragmented peptides derived from these polypeptides, and the uses of the above.



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Qy     269 ValThrPheHisTyrLysArgSerSerLeuSerTyrPheGluGlyValCysSerArgThr 288
           ||||||||||||||||||||||||||||||||||||||    ||||||||||||||||||
Db    1174 GTGACATTTCACTATAAGAGAAGCAGTCTGAGTTACTTTGGAGGTGTCTGTTCTCGCACA 1233

Qy     289 ArgGlyValGlyValAsnGluTyrGlyLeuProMetAlaValAlaGlnValLeuSerGln 308
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1234 AGAGGAGTTGGTGTGAATGAGTATGGTCTTCCAATGGCAGTGGCACAAGTATTATCGCAG 1293

Qy     309 SerLeuAlaGlnAsnLeuGlyIleGlnTrpGluProSerSerArgLysProLysCysAsp 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1294 AGCCTGGCTCAAAACCTTGGAATCCAATGGGAACCTTCTAGCAGAAAGCCAAAATGTGAC 1353

Qy     329 CysThrGluSerTrpGlyGlyCysIleMetGluGluThrGlyValSerHisSerArgLys 348
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1354 TGCACAGAATCCTGGGGTGGCTGCATCATGGAGGAAACAGGGGTGTCCCATTCTCGAAAA 1413

Qy     349 PheSerLysCysSerIleLeuGluTyrArgAspPheLeuGlnArgGlyGlyGlyAlaCys 368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1414 TTTTCAAAGTGCAGCATTTTGGAGTATAGAGACTTTTTACAGAGAGGAGGTGGAGCCTGC 1473
                                                   382
Qy     369 LeuPheAsnArgProThrLysLeuPheGluProThrGluCysGlyAsnGlyTyrValGlu 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1474 CTTTTCAACAGGCCAACAAAGCTATTTGAGCCCACGGAATGTGGAAATGGATACGTGGAA 1533

Qy     389 AlaGlyGluGluCysAspCysGlyPheHisValGluCysTyrGlyLeuCysCysLysLys 408
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1534 GCTGGGGAGGAGTGTGATTGTGGTTTTCATGTGGAATGCTATGGATTATGCTGTAAGAAA 1593

Qy     409 CysSerLeuSerAsnGlyAlaHisCysSerAspGlyProCysCysAsnAsnThrSerCys 428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1594 TGTTCCCTCTCCAACGGGGCTCACTGCAGCGACGGGCCCTGCTGTAACAATACCTCATGT 1653
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Qy     429 LeuPheGlnProArgGlyTyrGluCysArgAspAlaValAsnGluCysAspIleThrGlu 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1654 CTTTTTCAGCCACGAGGGTATGAATGCCGGGATGCTGTGAACGAGTGTGATATTACTGAA 1713
                                                             464
Qy     449 TyrCysThrGlyAspSerGlyGlnCysProProAsnLeuHisLysGlnAspGlyTyrAla 468
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1714 TATTGTACTGGAGACTCTGGTCAGTGCCCACCAAATCTTCATAAGCAAGACGGATATGCA 1773

Qy     469 CysAsnGlnAsnGlnGlyArgCysTyrAsnGlyGluCysLysThrArgAspAsnGlnCys 488
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1774 TGCAATCAAAATCAGGGCCGCTGCTACAATGGCGAGTGCAAGACCAGAGACAACCAGTGT 1833

Qy     489 GlnTyrIleTrpGlyThrLysAlaAlaGlySerAspLysPheCysTyrGluLysLeuAsn 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1834 CAGTACATCTGGGGAACAAAGGCTGCAGGGTCTGACAAGTTCTGCTATGAAAAGCTGAAT 1893

Qy     509 ThrGluGlyThrGluLysGlyAsnCysGlyLysAspGlyAspArgTrpIleGlnCysSer 528
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1894 ACAGAAGGCACTGAGAAGGGAAACTGCGGGAAGGATGGAGACCGGTGGATTCAGTGCAGC 1953

Qy     529 LysHisAspValPheCysGlyPheLeuLeuCysThrAsnLeuThrArgAlaProArgIle 548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1954 AAACATGATGTGTTCTGTGGATTCTTACTCTGTACCAATCTTACTCGAGCTCCACGTATT 2013

Qy     549 GlyGlnLeuGlnGlyGluIleIleProThrSerPheTyrHisGlnGlyArgValIleAsp 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2014 GGTCAACTTCAGGGTGAGATCATTCCAACTTCCTTCTACCATCAAGGCCGGGTGATTGAC 2073

Qy     569 CysSerGlyAlaHisValValLeuAspAspAspThrAspValGlyTyrValGluAspGly 588
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2074 TGCAGTGGTGCCCATGTAGTTTTAGATGATGATACGGATGTGGGCTATGTAGAAGATGGA 2133

Qy     589 ThrProCysGlyProSerMetMetCysLeuAspArgLysCysLeuGlnIleGlnAlaLeu 608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2134 ACGCCATGTGGCCCGTCTATGATGTGTTTAGATCGGAAGTGCCTACAAATTCAAGCCCTA 2193

Qy     609 AsnMetSerSerCysProLeuAspSerLysGlyLysValCysSerGlyHisGlyValCys 628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2194 AATATGAGCAGCTGTCCACTCGATTCCAAGGGTAAAGTCTGTTCGGGCCATGGGGTGTGT 2253

Qy     629 SerAsnGluAlaThrCysIleCysAspPheThrTrpAlaGlyThrAspCysSerIleArg 648
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2254 AGTAATGAAGCCACCTGCATTTGTGATTTCACCTGGGCAGGGACAGATTGCAGTATCCGG 2313

Qy     649 AspProValArgAsnLeuHisProProLysAspGluGlyProLysGly 664
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    2314 GATCCAGTTAGGAACCTTCACCCCCCCAAGGATGAAGGACCCAAGGGT 2361
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